Amendments to the claims:

1. (Currently Amended) A method for screening for transcription factor modulators, the method comprising:

forming a plurality of test samples by contacting samples of cells with different agents; and

for each test sample, identifying which of a plurality of different activated transcription factors are present by

taking a library of double stranded nucleic acid probes, the ~~transcription factor~~ nucleic acid probes each comprising a ~~predetermined~~ recognition sequence ~~capable of binding~~ that is known to bind to an activated known transcription factor~~, the recognition sequence~~ and ~~varying~~ varies within the library for binding to different activated known transcription factors,

contacting the test sample with the library of double stranded DNA probes under conditions where nucleic acid probe - transcription factor complexes are formed between the nucleic acid probes and activated transcription factors present in the test sample,

isolating the nucleic acid probes from the nucleic acid probe-transcription factor complexes formed, ~~and~~

contacting the isolated nucleic acid probes with an array of immobilized hybridization probes under conditions suitable for hybridization of the strands of the different double stranded nucleic acid probes to the hybridization probes in the array, and

comparing the activated known transcription factors present in the test sample with a control sample of cells not contacted with any of the different agents, the difference in the presence of transcription factors between the test and control sample being indicative of the transcription modulation by the agent contacted with the test sample; and

comparing the activated transcription factors present in the different test samples.

2. (Currently Amended) The method according to claims 1 wherein ~~at least 1%~~ each of the double stranded nucleic acid probes in the library ~~have~~ has a recognition ~~sequences~~ sequence greater than 35 base pairs in length.

3. (Currently Amended) The method according to claims 1 wherein ~~at least 1%~~ each of the double stranded nucleic acid probes in the library ~~have~~ has a recognition ~~sequences~~ sequence greater than 40 base pairs in length.

4. (Currently Amended) The method according to claims 1 wherein ~~at least 1%~~ each of the double stranded nucleic acid probes in the library ~~have~~ has a recognition ~~sequences~~ sequence greater than 45 base pairs in length.

5-7. (Canceled)

8. (Previously Presented) The method according to claims 1 wherein each of the recognition sequences has between 20 and 40 base pairs in length.

9. (Previously Presented) The method according to claims 1 wherein each of the recognition sequences has between 25 and 35 base pairs in length.

10. (Currently Amended) The method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 5 different ~~DNA~~ nucleic acid probes each having a different recognition ~~sequences~~ sequence.

11. (Currently Amended) The method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 10 different ~~DNA~~ nucleic acid probes each having a different recognition ~~sequences~~ sequence.

12. (Currently Amended) The method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 20 different ~~DNA~~ nucleic acid probes each having a different recognition ~~sequences~~ sequence.

13. (Currently Amended) The A method according to claims 1 wherein the library of double stranded nucleic acid probes comprises at least 50 different ~~DNA~~ nucleic acid probes each having a different recognition ~~sequences~~ sequence.

14. (Currently Amended) The method according to claims 1 wherein the ~~library comprises DNA~~ recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from at least 5 different types of cells.

15. (Currently Amended) The A method according to claims 1 wherein the ~~DNA~~ recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from at least 10 different types of cells.

16. (Previously Amended) The method according to claims 1 wherein the recognition sequences in the library of nucleic acid probes are for recognizing activated transcription factors from malignant, benign, and normal cell types.

17. (Previously Presented) The method according to claims 1 each of the immobilized hybridization probes on the array comprises at least two copies of a complement to a portion of a recognition sequence comprised on the nucleic acid probe.

18. (Currently Amended) The method according to claim 1, wherein the recognition sequences comprised on the nucleic acid probes are ~~predetermined~~ known to bind to two or more transcription factors selected from the group consisting of AP1, AP-2, ARE, Brn-3, C/EBP, CBF, CDP, c-Myb, CREB, E2F-1, EFR, ERE, Ets, Ets-1/PEA3, FAST-1, GAS/ISRE, GATA, GRE, HNF-4, IRF-1, MEF-1, MEF-2, Myc-Max, NF-1, NFATc, NF-E1, NF-E2, NFκB, Oct-1, p53, Pax-5, Pbx1, Pit 1, PPAR, PRE, RAR, RAR (DR-5), SIE, Smad SBE, Smad3/4, SP1, SRE, Stat1, Stat3, Stat4, Stat4, Stat5, Stat6, TFIID, TR, TR(DR-4), USF-1, VDR (DR-3), HSE, and MRE.

19. (Currently Amended) The method according to claim 1, wherein the recognition sequences comprised on the nucleic acid probes are ~~predetermined~~ known to bind to two or more transcription factors selected from the group consisting of NF-E1, NFκB, Ets, Ap1, p53 and c-Myb.